For SN: 10/705,721

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Kahn M?/au
L1      .  3514 KAHN M?/AU

=> s l1 and site specific
L2          13 L1 AND SITE SPECIFIC

=> s l2 and (clon### or recombinat###)
L3          10 L2 AND (CLON### OR RECOMBINAT###)

=> dup rem l3
PROCESSING COMPLETED FOR L3
L4            6 DUP REM L3 (4 DUPLICATES REMOVED)

=> d l4 1-6 bib ab kwic

L4   ANSWER 1 OF 6  CAPLUS  COPYRIGHT 2006 ACS on STN
AN   2004:703109  CAPLUS
DN   141:201281
TI   Method for cloning PCR products without restriction or ligation
     enzymes
IN   Kahn, Michael L.; House, Brent L.
PA   USA
SO   U.S. Pat. Appl. Publ., 8 pp.
     CODEN: USXXCO
DT   Patent
LA   English
FAN.CNT 1
     PATENT NO.          KIND   DATE        APPLICATION NO.        DATE
     ---------------     ----   --------    --------------------   --------
PI   US 2004166512        A1    20040826    US 2003-705721         20031110
PRAI US 2002-425955P      P     20021112
AB   In one aspect the invention provides methods for cloning
     polymerase chain reaction (PCR) products without the need for restriction
     enzymes, ligation enzymes, or DNA purification steps.  According to these
     methods, a PCR product is transferred into a vector in vivo using a
     site-specific recombination system.  In some
     embodiments, the methods include the steps of (1) providing a PCR product
     flanked by a first site-specific recombination
     site and a second site-specific recombination
     site; and (2) transferring the PCR product into a cell comprising a target
     sequence flanked by a first recombination site partner and a
     second recombination site partner, and at least one
     recombination protein that mediates recombination
     between the first site-specific recombination
     site and the first recombination site partner, and between the
     second site-specific recombination site and
     the second recombination site partner.
TI   Method for cloning PCR products without restriction or ligation
     enzymes
IN   Kahn, Michael L.; House, Brent L.
AB   In one aspect the invention provides methods for cloning
     polymerase chain reaction (PCR) products without the need for restriction
     enzymes, ligation enzymes, or DNA purification steps.  According to these
     methods, a PCR product is transferred into a vector in vivo using a
     site-specific recombination system.  In some
     embodiments, the methods include the steps of (1) providing a PCR product
     flanked by a first site-specific recombination
     site and a second site-specific recombination
     site; and (2) transferring the PCR product into a cell comprising a target
     sequence flanked by a first recombination site partner and a
     second recombination site partner, and at least one
     recombination protein that mediates recombination
     between the first site-specific recombination
     site and the first recombination site partner, and between the
     second site-specific recombination site and
     the second recombination site partner.
ST   integration recombination PCR restriction ligation enzyme
IT   Proteins
     RL: BUU (Biological use, unclassified); BIOL (Biological study); USES
```

(Uses)
(IHF (integration host factor); method for **cloning** PCR products without restriction or ligation enzymes)

IT Escherichia coli
Eubacteria
(as expression host; method for **cloning** PCR products without restriction or ligation enzymes)

IT Genetic element
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(attB, attB1 or attB2 site; method for **cloning** PCR products without restriction or ligation enzymes)

IT Genetic element
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(attP, attP2 or attP1 site; method for **cloning** PCR products without restriction or ligation enzymes)

IT **Recombination**, genetic
(integration; method for **cloning** PCR products without restriction or ligation enzymes)

IT Coliphage λ
Genetic vectors
Genome
Molecular **cloning**
PCR (polymerase chain reaction)
Plasmids
(method for **cloning** PCR products without restriction or ligation enzymes)

IT Primers (nucleic acid)
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(method for **cloning** PCR products without restriction or ligation enzymes)

IT 52350-85-3P, Integrase
RL: BPN (Biosynthetic preparation); BUU (Biological use, unclassified); BIOL (Biological study); PREP (Preparation); USES (Uses)
(method for **cloning** PCR products without restriction or ligation enzymes)

IT 740984-78-5 740984-79-6 740984-80-9 740984-81-0
RL: PRP (Properties)
(unclaimed nucleotide sequence; method for **cloning** PCR products without restriction or ligation enzymes)

L4 ANSWER 2 OF 6 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:610609 CAPLUS
DN 139:160795
TI Methods and vectors for facilitating **site-specific recombination**
IN **Kahn, Michael L.**; House, Brent L.; Mortimer, Michael W.
PA Washington State University Research Foundation, USA
SO PCT Int. Appl., 52 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2003064623	A2	20030807	WO 2003-US3176	20030131
	WO 2003064623	A3	20040318		
	W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW				
	RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
	US 2003219902	A1	20031127	US 2003-357268	20030131
PRAI	US 2002-354063P	P	20020131		

AB Te invention provides methods for moving an insert nucleic acid mol. between vectors using **site-specific recombination** in vivo. In another aspect, the invention provides methods for the functional anal. of a genome using **site-specific recombination** in vivo. Another aspect of the invention provides methods for deleting a target genomic region by intra-mol. **site-specific recombination**. Further aspects provide vectors and kits for use in the methods of the invention. The invention provides methods and vectors for analyzing a genome of bacteria such as Sinorhizobium meliloti by **site-specific recombination** in-vivo. The **recombination** sites comprise FRT sequences and the **recombination** proteins comprise a Flp recombinase. The prototypical **site-specific recombination** is used to integrate bacteriophage λ into E. coli genome.

TI Methods and vectors for facilitating **site-specific recombination**

IN **Kahn, Michael L.**; House, Brent L.; Mortimer, Michael W.

AB Te invention provides methods for moving an insert nucleic acid mol. between vectors using **site-specific recombination** in vivo. In another aspect, the invention provides methods for the functional anal. of a genome using **site-specific recombination** in vivo. Another aspect of the invention provides methods for deleting a target genomic region by intra-mol. **site-specific recombination**. Further aspects provide vectors and kits for use in the methods of the invention. The invention provides methods and vectors for analyzing a genome of bacteria such as Sinorhizobium meliloti by **site-specific recombination** in-vivo. The **recombination** sites comprise FRT sequences and the **recombination** proteins comprise a Flp recombinase. The prototypical **site-specific recombination** is used to integrate bacteriophage λ into E. coli genome.

ST Escherichia plasmid RK2 oriT sequence **cloning** vector **recombination**

IT Plasmids
(ColE1; methods and vectors for facilitating **site-specific recombination**)

IT Enzymes, biological studies
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(DNA-recombining, gene FLP; methods and vectors for facilitating **site-specific recombination**)

IT Genetic element
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(FRT sites; methods and vectors for facilitating **site-specific recombination**)

IT Gene, microbial
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(FRT; methods and vectors for facilitating **site-specific recombination**)

IT Proteins
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(IHF (integration host factor); methods and vectors for facilitating **site-specific recombination**)

IT Plasmids
(RK2; methods and vectors for facilitating **site-specific recombination**)

IT Proteins
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(Xis; methods and vectors for facilitating **site-specific recombination**)

IT Genetic element
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(attB, attB2; methods and vectors for facilitating **site-specific recombination**)

IT Genetic element
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(attL, attL2; methods and vectors for facilitating **site-specific recombination**)

IT Genetic element
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(attP, attP1 an attP2 sites; methods and vectors for facilitating **site-specific recombination**)
IT Genetic element
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(attR, attR1 and attR2 site; methods and vectors for facilitating **site-specific recombination**)
IT Genetic element
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(attenuator; methods and vectors for facilitating **site-specific recombination**)
IT Gene, microbial
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(ccdB; methods and vectors for facilitating **site-specific recombination**)
IT **Recombination**, genetic
(homologous; methods and vectors for facilitating **site-specific recombination**)
IT Coliphage λ
Conjugation (genetic)
DNA sequences
Escherichia coli
Eubacteria
Genetic vectors
Molecular **cloning**
Prokaryota
Recombination, genetic
Sinorhizobium meliloti
Test kits
(methods and vectors for facilitating **site-specific recombination**)
IT DNA
Nucleic acids
Promoter (genetic element)
Reporter gene
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(methods and vectors for facilitating **site-specific recombination**)
IT Genetic element
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(oriT, of plasmid RK2; methods and vectors for facilitating **site-specific recombination**)
IT **Recombination**, genetic
(**site-specific**; methods and vectors for facilitating **site-specific recombination**)
IT 573748-79-5, DNA (Escherichia coli plasmid RK2)
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(nucleotide sequence; methods and vectors for facilitating **site-specific recombination**)
IT 573767-79-0 573767-80-3 573767-81-4 573767-82-5
RL: PRP (Properties)
(unclaimed nucleotide sequence; methods and vectors for facilitating **site-specific recombination**)

L4 ANSWER 3 OF 6 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:634532 CAPLUS
DN 136:242628
TI Nucleotide sequence and predicted functions of the entire Sinorhizobium meliloti pSymA megaplasmid
AU Barnett, Melanie J.; Fisher, Robert F.; Jones, Ted; Komp, Caridad; Abola, A. Pia; Barloy-Hubler, Frederique; Bowser, Leah; Capela, Delphine; Galibert, Francis; Gouzy, Jerome; Gurjal, Mani; Hong, Andrea; Huizar, Lucas; Hyman, Richard W.; Kahn, Daniel; **Kahn, Michael L.**; Kalman, Sue; Keating, David H.; Palm, Curtis; Peck, Melicent C.; Surzycki, Raymond; Wells, Derek H.; Yeh, Kuo-Chen; Davis, Ronald W.; Federspiel, Nancy A.; Long, Sharon R.
CS Department of Biological Sciences, Stanford University, Stanford, CA,

94305, USA
SO Proceedings of the National Academy of Sciences of the United States of America (2001), 98(17), 9883-9888
CODEN: PNASA6; ISSN: 0027-8424
PB National Academy of Sciences
DT Journal
LA English
AB The symbiotic nitrogen-fixing soil bacterium Sinorhizobium meliloti contains three replicons: pSymA, pSymB, and the chromosome. We report here the complete 1354,226-nt sequence of pSymA. In addition to a large fraction of the genes known to be specifically involved in symbiosis, pSymA contains genes likely to be involved in nitrogen and carbon metabolism, transport, stress, and resistance responses, and other functions that give S. meliloti an advantage in its specialized niche.
RE.CNT 72 THERE ARE 72 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT
AU Barnett, Melanie J.; Fisher, Robert F.; Jones, Ted; Komp, Caridad; Abola, A. Pia; Barloy-Hubler, Frederique; Bowser, Leah; Capela, Delphine; Galibert, Francis; Gouzy, Jerome; Gurjal, Mani; Hong, Andrea; Huizar, Lucas; Hyman, Richard W.; Kahn, Daniel; **Kahn, Michael L.**; Kalman, Sue; Keating, David H.; Palm, Curtis; Peck, Melicent C.; Surzycki, Raymond; Wells, Derek H.; Yeh, Kuo-Chen; Davis, Ronald W.; Federspiel, Nancy A.; Long, Sharon R.
IT Gene, microbial
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(SMa1289; **nucleotide sequence** and predicted functions of entire Sinorhizobium meliloti pSymA megaplasmid)
IT Gene, microbial
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(SMa1833; **nucleotide** sequence and predicted functions of entire Sinorhizobium meliloti pSymA megaplasmid)
IT Gene, microbial
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(SMa1835; nucleotide sequence **and** predicted functions of entire Sinorhizobium meliloti pSymA megaplasmid)
IT Gene, microbial
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(SMa1838; nucleotide sequence **and** predicted functions of entire Sinorhizobium meliloti pSymA megaplasmid)
IT Gene, microbial
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(SMa1844; **nucleotide** sequence and predicted functions of entire Sinorhizobium meliloti pSymA megaplasmid)
IT Gene, microbial
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(SMa1846; nucleotide sequence and predicted **functions** of entire Sinorhizobium meliloti pSymA megaplasmid)
IT Gene, microbial
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(SMa1850; nucleotide sequence **and** predicted functions of entire Sinorhizobium meliloti pSymA megaplasmid)
IT 97048-32-3, Protein (Rhizobium meliloti **clone** pRmSL26 gene nodC reduced) 124247-24-1, Protein (Rhizobium meliloti plasmid pSym **clone** pDD27 gene fixS) 124248-18-6, Protein (Rhizobium meliloti plasmid pSym **clone** pDD27 gene fixH) 124248-46-0 124833-97-2, Protein (Rhizobium meliloti **clone** pDK85 reduced) 130428-86-3, RNA formation factor (Rhizobium meliloti plasmid pSym **clone** pMB1 gene syrM reduced) 136253-39-9, RNA formation factor (Rhizobium meliloti **clone** pBGR2 gene nodD3 reduced) 192589-22-3 204785-58-0
204785-59-1 353833-17-7 353833-18-8 353833-19-9 353833-20-2
353833-21-3 353833-22-4 353833-23-5 353833-25-7 353833-26-8
353833-27-9 353833-28-0 353833-29-1 353833-30-4 353833-31-5

353833-32-6 353833-33-7 353833-34-8 353833-35-9 353833-36-0
353833-37-1 353833-38-2 353833-39-3 353833-40-6 353833-41-7
353833-42-8 353833-43-9 353833-44-0 353833-45-1 353833-46-2
353833-47-3 353833-48-4 353833-49-5 353833-50-8 353833-51-9
353833-52-0 353833-53-1 353833-54-2 353833-55-3 353833-56-4
353833-57-5 353833-58-6 353833-59-7 353833-60-0 353833-61-1
353833-62-2 353833-63-3 353833-64-4 353833-65-5 353833-66-6
353833-67-7 353833-68-8 353833-69-9 353833-70-2 353833-71-3
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353833-77-9 353833-78-0 353833-79-1 353833-80-4 353833-81-5
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353833-92-8 353833-93-9 353833-94-0 353833-95-1 353833-96-2
353833-97-3 353833-98-4 353833-99-5 353834-00-1 353834-01-2
353834-02-3 353834-03-4 353834-04-5 353834-05-6 353834-06-7
353834-07-8 353834-08-9 353834-09-0 353834-10-3 353834-11-4
353834-12-5 353834-13-6 353834-14-7 353834-15-8 353834-16-9
353834-17-0 353834-18-1 353834-19-2 353834-20-5 353834-21-6
353834-22-7 353834-23-8 353834-24-9 353834-25-0 353834-26-1
353834-27-2 353834-28-3 353834-29-4 353834-30-7 353834-31-8
353834-32-9 353834-33-0 353834-34-1 353834-35-2 353834-36-3
353834-37-4 353834-38-5 353834-39-6 353834-40-9 353834-41-0
353834-42-1 353834-43-2 353834-44-3 353834-45-4 353834-46-5
353834-47-6 353834-48-7 353834-49-8 353834-50-1 353834-51-2
353834-52-3 353834-53-4 353834-54-5 353834-55-6 353834-56-7
353834-57-8 353834-58-9 353834-59-0 353834-60-3 353834-61-4
353834-62-5 353834-63-6 353834-64-7 353834-65-8 353834-66-9
353834-67-0 353834-68-1 353834-69-2 353834-70-5 353834-71-6
353834-72-7 353834-73-8 353834-74-9 353834-75-0 353834-76-1
353834-77-2 353834-78-3 353834-79-4 353834-80-7 353834-81-8
353834-82-9 353834-83-0 353834-84-1 353834-85-2 353834-86-3
353834-87-4 353834-88-5 353834-89-6 353834-90-9 353834-91-0
353834-92-1 353834-93-2 353834-94-3 353834-95-4 353834-96-5
353834-97-6 353834-98-7 353834-99-8 353835-00-4 353835-01-5
353835-02-6 353835-03-7 353835-04-8 353835-05-9 353835-06-0
353835-07-1 353835-08-2 353835-09-3 353835-10-6 353835-11-7
353835-12-8 353835-13-9 353835-14-0 353835-15-1 353835-16-2
353835-17-3 353835-18-4 353835-19-5 353835-20-8 353835-21-9
353835-22-0 353835-23-1 353835-24-2 353835-25-3 353835-26-4
353835-27-5 353835-28-6 353835-29-7 353835-30-0 353835-31-1
353835-32-2 353835-33-3 353835-34-4 353835-35-5 353835-36-6
353835-37-7 353835-38-8 353835-39-9 353835-40-2 353835-41-3
353835-42-4 353835-43-5 353835-44-6
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; nucleotide sequence and predicted functions of entire Sinorhizobium meliloti pSymA megaplasmid)

L4 ANSWER 4 OF 6 CAPLUS COPYRIGHT 2006 ACS on STN DUPLICATE 1
AN 1988:107184 CAPLUS
DN 108:107184
TI Integration of satellite bacteriophage P4 in Escherichia coli. DNA sequences of the phage and host regions involved in **site-specific recombination**
AU Pierson, L. S., III; **Kahn, M. L.**
CS Dep. Microbiol., Washington State Univ., Pullman, WA, 99164, USA
SO Journal of Molecular Biology (1987), 196(3), 487-96 order
CODEN: JMOBAK; ISSN: 0022-2836
DT Journal
LA English
AB The DNA sequences of regions essential for phage P4 integration were determined A 20-base-pair core sequence in both phage (P4attP) and host (P4attB) attachment regions contains the **recombination** site. In P4attP, this sequence is flanked by 5 repeated sequences. A 1.3 + 103-base open reading frame codes for P4 integrase. Two possible promoters are upstream from P4int. One would be recognized by Escherichia coli RNA polymerase and may be repressed by integrase protein. The second would be recognized by RNA polymerase modified after infection by a P4 helper phase, P2. The P4attB core sequence is the 3' end of a leucine tRNA gene.

Downstream from this tRNA in E. coli K-12 is a region homologous to P4int that may be part of a cryptic prophage.

TI Integration of satellite bacteriophage P4 in Escherichia coli. DNA sequences of the phage and host regions involved in **site-specific recombination**

AU Pierson, L. S., III; **Kahn, M. L.**

AB The DNA sequences of regions essential for phage P4 integration were determined A 20-base-pair core sequence in both phage (P4attP) and host (P4attB) attachment regions contains the **recombination** site. In P4attP, this sequence is flanked by 5 repeated sequences. A 1.3 + 103-base open reading frame codes for P4 integrase. Two possible promoters are upstream from P4int. One would be recognized by Escherichia coli RNA polymerase and may be repressed by integrase protein. The second would be recognized by RNA polymerase modified after infection by a P4 helper phase, P2. The P4attB core sequence is the 3' end of a leucine tRNA gene. Downstream from this tRNA in E. coli K-12 is a region homologous to P4int that may be part of a cryptic prophage.

ST phage P4 DNA **recombination** sequence Escherichia; integrase gene sequence phage P4

IT **Recombination**, genetic
(**site-specific**, of prophage P4, in Escherichia coli DNA)

L4 ANSWER 5 OF 6 CAPLUS COPYRIGHT 2006 ACS on STN DUPLICATE 2

AN 1986:203037 CAPLUS

DN 104:203037

TI The integrase family of **site-specific** recombinases: regional similarities and global diversity

AU Argos, Patrick; Landy, Arthur; Abremski, Kenneth; Egan, J. Barry; Haggard-Ljungquist, Elisabeth; Hoess, Ronald H.; **Kahn, Michael L.** ; Kalionis, Bill; Narayana, S. V. L.; et al.

CS Eur. Mol. Biol. Lab., Heidelberg, D-6900, Fed. Rep. Ger.

SO EMBO Journal (1986), 5(2), 433-40
CODEN: EMJODG; ISSN: 0261-4189

DT Journal

LA English

AB A combination of 2 methods for detecting distant relationships in protein primary sequences was used to compare the **site-specific recombination** proteins encoded by bacteriophages λ, .vphi.80, P22, P2, 186, P4, and P1. This group of proteins exhibits an unexpectedly large diversity of sequences. Despite this diversity, all of the recombinases can be aligned in their C-terminal halves. A 40-residue region near the C terminus is particularly well conserved in all the proteins and is homologous to a region near the C terminus of the yeast 2μ plasmid Flp protein. This family of recombinases does not appeär to be related to any other **site-specific** recombinases.
Three positions are perfectly conserved within this family: histidine, arginine, and tyrosine are found at resp. alignment positions 396, 399, and 433 within the well-conserved C-terminal region. These residues may contribute to the active site of this family of recombinases, and tyrosine-433 may form a transient covalent linkage to DNA during strand cleavage and rejoining.

TI The integrase family of **site-specific** recombinases: regional similarities and global diversity

AU Argos, Patrick; Landy, Arthur; Abremski, Kenneth; Egan, J. Barry; Haggard-Ljungquist, Elisabeth; Hoess, Ronald H.; **Kahn, Michael L.** ; Kalionis, Bill; Narayana, S. V. L.; et al.

AB A combination of 2 methods for detecting distant relationships in protein primary sequences was used to compare the **site-specific recombination** proteins encoded by bacteriophages λ, .vphi.80, P22, P2, 186, P4, and P1. This group of proteins exhibits an unexpectedly large diversity of sequences. Despite this diversity, all of the recombinases can be aligned in their C-terminal halves. A 40-residue region near the C terminus is particularly well conserved in all the proteins and is homologous to a region near the C terminus of the yeast 2μ plasmid Flp protein. This family of recombinases does not appear to be related to any other **site-specific** recombinases.
Three positions are perfectly conserved within this family: histidine, arginine, and tyrosine are found at resp. alignment positions 396, 399,

and 433 within the well-conserved C-terminal region. These residues may contribute to the active site of this family of recombinases, and tyrosine-433 may form a transient covalent linkage to DNA during strand cleavage and rejoining.

L4 ANSWER 6 OF 6 MEDLINE on STN
AN 82028653 MEDLINE
DN PubMed ID: 6269959
TI The nucleotide sequence of IS5 from Escherichia coli.
AU Schoner B; **Kahn M**
NC 5-T32-CA09139 (NCI)
GM07189 (NIGMS)
PO1-CA16519 (NCI)
SO Gene, (1981 Aug) Vol. 14, No. 3, pp. 165-74.
Journal code: 7706761. ISSN: 0378-1119.
CY Netherlands
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
OS GENBANK-J01734
EM 198112
ED Entered STN: 19900316
Last Updated on STN: 19990129
Entered Medline: 19811221
AB A 3-kb fragment of Haemophilus haemolyticus DNA which carries the HhaII restriction (r) and modification (m) genes has been **cloned** into the PstI site of pBR322 (Mann et al., 1978). When propagated in Escherichia coli, it was observed that spontaneous insertions of IS5 inactivated the restriction gene, producing r- mutants at a frequency of 10(-6). Electron microscopy, restriction-site mapping and sequence analysis of two r- plasmids have demonstrated the presence of IS5 at a single target site in both possible orientations. The complete nucleotide sequence of IS5 has been determined. It is 1195 bp long and has inverted terminal repeats of 16 bp. The target site for IS5 in this plasmid is 5'-CTAG. Approx. ten copies of IS5 were found to be present at about the same locations on the E. coli chromosome in various K-12 strains, using Southern hybridization analysis.
AU Schoner B; **Kahn M**
AB A 3-kb fragment of Haemophilus haemolyticus DNA which carries the HhaII restriction (r) and modification (m) genes has been **cloned** into the PstI site of pBR322 (Mann et al., 1978). When propagated in Escherichia coli, it was observed that spontaneous. . .
CT Base Sequence
*DNA Restriction Enzymes: GE, genetics
*DNA Transposable Elements
*DNA, Bacterial: AN, analysis
DNA, Recombinant: ME, metabolism
***Deoxyribonucleases, Type II Site-Specific**
*Escherichia coli: GE, genetics
Microscopy, Electron
Mutation
Plasmids
Research Support, Non-U.S. Gov't
Research Support, U.S. Gov't, P.H.S.
CN. . . Bacterial); 0 (DNA, Recombinant); 0 (Plasmids); EC 3.1.21 (DNA Restriction Enzymes); EC 3.1.21.- (endodeoxyribonuclease HinfI); EC 3.1.21.4 (Deoxyribonucleases, Type II **Site-Specific**)

=> s house B?/au
L5 100 HOUSE B?/AU

=> s l5 and (clon### or recombinat###)
L6 11 L5 AND (CLON### OR RECOMBINAT###)

=> s l6 and in vivo
L7 9 L6 AND IN VIVO

=> s l7 and specific

```
L8          6 L7 AND SPECIFIC

=>·s l8 and site#
L9          2 L8 AND SITE#

=> d l9 1-2 bib ab kwic

L9   ANSWER 1 OF 2  CAPLUS  COPYRIGHT 2006 ACS on STN
AN   2004:703109  CAPLUS
DN   141:201281
TI   Method for cloning PCR products without restriction or ligation
     enzymes
IN   Kahn, Michael L.; House, Brent L.
PA   USA
SO   U.S. Pat. Appl. Publ., 8 pp.
     CODEN: USXXCO
DT   Patent
LA   English
FAN.CNT 1
     PATENT NO.          KIND   DATE        APPLICATION NO.         DATE
     --------------      ----   --------    --------------------    --------
PI   US 2004166512        A1    20040826    US 2003-705721          20031110
PRAI US 2002-425955P      P     20021112
AB   In one aspect the invention provides methods for cloning
     polymerase chain reaction (PCR) products without the need for restriction
     enzymes, ligation enzymes, or DNA purification steps.  According to these
     methods, a PCR product is transferred into a vector in vivo
     using a site-specific recombination system.
     In some embodiments, the methods include the steps of (1) providing a PCR
     product flanked by a first site-specific
     recombination site and a second site-
     specific recombination site; and (2)
     transferring the PCR product into a cell comprising a target sequence
     flanked by a first recombination site partner and a
     second recombination site partner, and at least one
     recombination protein that mediates recombination
     between the first site-specific recombination
     site and the first recombination site partner,
     and between the second site-specific
     recombination site and the second recombination
     site partner.
TI   Method for cloning PCR products without restriction or ligation
     enzymes
IN   Kahn, Michael L.; House, Brent L.
AB   In one aspect the invention provides methods for cloning
     polymerase chain reaction (PCR) products without the need for restriction
     enzymes, ligation enzymes, or DNA purification steps.  According to these
     methods, a PCR product is transferred into a vector in vivo
     using a site-specific recombination system.
     In some embodiments, the methods include the steps of (1) providing a PCR
     product flanked by a first site-specific
     recombination site and a second site-
     specific recombination site; and (2)
     transferring the PCR product into a cell comprising a target sequence
     flanked by a first recombination site partner and a
     second recombination site partner, and at least one
     recombination protein that mediates recombination
     between the first site-specific recombination
     site and the first recombination site partner,
     and between the second site-specific
     recombination site and the second recombination
     site partner.
ST   integration recombination PCR restriction ligation enzyme
IT   Proteins
     RL: BUU (Biological use, unclassified); BIOL (Biological study); USES
     (Uses)
        (IHF (integration host factor); method for cloning PCR
        products without restriction or ligation enzymes)
IT   Escherichia coli
```

Eubacteria
(as expression host; method for **cloning** PCR products without restriction or ligation enzymes)

IT Genetic element
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(attB, attB1 or attB2 **site**; method for **cloning** PCR products without restriction or ligation enzymes)

IT Genetic element
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(attP, attP2 or attP1 **site**; method for **cloning** PCR products without restriction or ligation enzymes)

IT **Recombination**, genetic
(integration; method for **cloning** PCR products without restriction or ligation enzymes)

IT Coliphage λ
Genetic vectors
Genome
Molecular **cloning**
PCR (polymerase chain reaction)
Plasmids
(method for **cloning** PCR products without restriction or ligation enzymes)

IT Primers (nucleic acid)
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(method for **cloning** PCR products without restriction or ligation enzymes)

IT 52350-85-3P, Integrase
RL: BPN (Biosynthetic preparation); BUU (Biological use, unclassified); BIOL (Biological study); PREP (Preparation); USES (Uses)
(method for **cloning** PCR products without restriction or ligation enzymes)

IT 740984-78-5 740984-79-6 740984-80-9 740984-81-0
RL: PRP (Properties)
(unclaimed nucleotide sequence; method for **cloning** PCR products without restriction or ligation enzymes)

L9 ANSWER 2 OF 2 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:610609 CAPLUS
DN 139:160795
TI Methods and vectors for facilitating **site-specific recombination**
IN Kahn, Michael L.; **House, Brent L.**; Mortimer, Michael W.
PA Washington State University Research Foundation, USA
SO PCT Int. Appl., 52 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2003064623	A2	20030807	WO 2003-US3176	20030131
	WO 2003064623	A3	20040318		
	W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW				
	RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
	US 2003219902	A1	20031127	US 2003-357268	20030131
PRAI	US 2002-354063P	P	20020131		

AB Te invention provides methods for moving an insert nucleic acid mol. between vectors using **site-specific recombination** in **vivo**. In another aspect, the invention provides methods for the functional anal. of a genome using **site**

-**specific recombination** in **vivo**. Another aspect of the invention provides methods for deleting a target genomic region by intra-mol. **site-specific recombination**. Further aspects provide vectors and kits for use in the methods of the invention. The invention provides methods and vectors for analyzing a genome of bacteria such as Sinorhizobium meliloti by **site-specific recombination** in-**vivo**. The **recombination sites** comprise FRT sequences and the **recombination** proteins comprise a Flp recombinase. The prototypical **site-specific recombination** is used to integrate bacteriophage λ into E. coli genome.

TI Methods and vectors for facilitating **site-specific recombination**

IN Kahn, Michael L.; **House, Brent L.**; Mortimer, Michael W.

AB Te invention provides methods for moving an insert nucleic acid mol. between vectors using **site-specific recombination** in **vivo**. In another aspect, the invention provides methods for the functional anal. of a genome using **site-specific recombination** in **vivo**. Another aspect of the invention provides methods for deleting a target genomic region by intra-mol. **site-specific recombination**. Further aspects provide vectors and kits for use in the methods of the invention. The invention provides methods and vectors for analyzing a genome of bacteria such as Sinorhizobium meliloti by **site-specific recombination** in-**vivo**. The **recombination sites** comprise FRT sequences and the **recombination** proteins comprise a Flp recombinase. The prototypical **site-specific recombination** is used to integrate bacteriophage λ into E. coli genome.

ST Escherichia plasmid RK2 oriT sequence **cloning** vector **recombination**

IT Plasmids
(ColE1; methods and vectors for facilitating **site-specific recombination**)

IT Enzymes, biological studies
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(DNA-recombining, gene FLP; methods and vectors for facilitating **site-specific recombination**)

IT Genetic element
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(FRT **sites**; methods and vectors for facilitating **site-specific recombination**)

IT Gene, microbial
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(FRT; methods and vectors for facilitating **site-specific recombination**)

IT Proteins
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(IHF (integration host factor); methods and vectors for facilitating **site-specific recombination**)

IT Plasmids
(RK2; methods and vectors for facilitating **site-specific recombination**)

IT Proteins
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(Xis; methods and vectors for facilitating **site-specific recombination**)

IT Genetic element
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(attB, attB2; methods and vectors for facilitating **site-specific recombination**)

IT Genetic element
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(attL, attL2; methods and vectors for facilitating **site-specific recombination**)

IT Genetic element
RL: BSU (Biological study, unclassified); BIOL (Biological study)

(attP, attP1 an attP2 **sites**; methods and vectors for facilitating **site-specific recombination**)
IT Genetic element
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(attR, attR1 and attR2 **site**; methods and vectors for facilitating **site-specific recombination**)
IT Genetic element
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(attenuator; methods and vectors for facilitating **site-specific recombination**)
IT Gene, microbial
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(ccdB; methods and vectors for facilitating **site-specific recombination**)
IT **Recombination**, genetic
(homologous; methods and vectors for facilitating **site-specific recombination**)
IT Coliphage λ
Conjugation (genetic)
DNA sequences
Escherichia coli
Eubacteria
Genetic vectors
Molecular **cloning**
Prokaryota
Recombination, genetic
Sinorhizobium meliloti
Test kits
(methods and vectors for facilitating **site-specific recombination**)
IT DNA
Nucleic acids
Promoter (genetic element)
Reporter gene
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(methods and vectors for facilitating **site-specific recombination**)
IT Genetic element
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(oriT, of plasmid RK2; methods and vectors for facilitating **site-specific recombination**)
IT **Recombination**, genetic
(**site-specific**; methods and vectors for facilitating **site-specific recombination**)
IT 573748-79-5, DNA (Escherichia coli plasmid RK2)
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(nucleotide sequence; methods and vectors for facilitating **site-specific recombination**)
IT 573767-79-0 573767-80-3 573767-81-4 573767-82-5
RL: PRP (Properties)
(unclaimed nucleotide sequence; methods and vectors for facilitating **site-specific recombination**)

=> dup rem l7
PROCESSING COMPLETED FOR L7
L10 4 DUP REM L7 (5 DUPLICATES REMOVED)

=> d l10 1-4 bib ab kwic

L10 ANSWER 1 OF 4 CAPLUS COPYRIGHT 2006 ACS on STN DUPLICATE 1
AN 2005:1120743 CAPLUS
DN 144:32786
TI Development of a functional genomics platform for Sinorhizobium meliloti: Construction of an ORFeome
AU Schroeder, Brenda K.; **House, Brent L.**; Mortimer, Michael W.; Yurgel, Svetlana N.; Maloney, Scott C.; Ward, Kristel L.; Kahn, Michael L.
CS Institute of Biological Chemistry, Washington State University, Pullman,

WA, 99164-6340, USA
SO Applied and Environmental Microbiology (2005), 71(10), 5858-5864
CODEN: AEMIDF; ISSN: 0099-2240
PB American Society for Microbiology
DT Journal
LA English
AB The nitrogen-fixing, symbiotic bacterium Sinorhizobium meliloti reduces mol. dinitrogen to ammonia in a specific symbiotic context, supporting the nitrogen requirements of various forage legumes, including alfalfa. Determining the DNA sequence of the S. meliloti genome was an important step in plant-microbe interaction research, adding to the considerable information already available about this bacterium by suggesting possible functions for many of the >6,200 annotated open reading frames (ORFs). However, the predictive power of bioinformatic anal. is limited, and putting the role of these genes into a biol. context will require more definitive functional approaches. We present here a strategy for genetic anal. of S. meliloti on a genomic scale and report the successful implementation of the first step of this strategy by constructing a set of plasmids representing 100% of the 6,317 annotated ORFs **cloned** into a mobilizable plasmid by using efficient PCR and **recombination** protocols. By using integrase **recombination** to insert these ORFs into other plasmids in vitro or in **vivo**, this ORFeome can be used to generate various specialized genetic materials for functional anal. of S. meliloti, such as operon fusions, mutants, and protein expression plasmids. The strategy can be generalized to many other genome projects, and the S. meliloti **clones** should be useful for investigators wanting an accessible source of **cloned** genes encoding specific enzymes.
RE.CNT 26 THERE ARE 26 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT
AU Schroeder, Brenda K.; **House, Brent L.**; Mortimer, Michael W.; Yurgel, Svetlana N.; Maloney, Scott C.; Ward, Kristel L.; Kahn, Michael L.
AB The nitrogen-fixing, symbiotic bacterium Sinorhizobium meliloti reduces mol. dinitrogen to ammonia in a specific symbiotic context, supporting the nitrogen requirements of various forage legumes, including alfalfa. Determining the DNA sequence of the S. meliloti genome was an important step in plant-microbe interaction research, adding to the considerable information already available about this bacterium by suggesting possible functions for many of the >6,200 annotated open reading frames (ORFs). However, the predictive power of bioinformatic anal. is limited, and putting the role of these genes into a biol. context will require more definitive functional approaches. We present here a strategy for genetic anal. of S. meliloti on a genomic scale and report the successful implementation of the first step of this strategy by constructing a set of plasmids representing 100% of the 6,317 annotated ORFs **cloned** into a mobilizable plasmid by using efficient PCR and **recombination** protocols. By using integrase **recombination** to insert these ORFs into other plasmids in vitro or in **vivo**, this ORFeome can be used to generate various specialized genetic materials for functional anal. of S. meliloti, such as operon fusions, mutants, and protein expression plasmids. The strategy can be generalized to many other genome projects, and the S. meliloti **clones** should be useful for investigators wanting an accessible source of **cloned** genes encoding specific enzymes.
ST bioinformatics Sinorhizobium ORFeome **cloning** algorithm database
IT Algorithm
Bioinformatics
Databases
Genome
Molecular **cloning**
Recombination, genetic
Sinorhizobium meliloti
(genomics platform for Sinorhizobium meliloti and construction of an ORFeome)

L10 ANSWER 2 OF 4 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2004:703109 CAPLUS
DN 141:201281
TI Method for **cloning** PCR products without restriction or ligation

enzymes
IN Kahn, Michael L.; **House, Brent L.**
PA USA
SO U.S. Pat. Appl. Publ., 8 pp.
CODEN: USXXCO
DT Patent
LA English
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI US 2004166512	A1	20040826	US 2003-705721	20031110
PRAI US 2002-425955P	P	20021112		

AB In one aspect the invention provides methods for **cloning** polymerase chain reaction (PCR) products without the need for restriction enzymes, ligation enzymes, or DNA purification steps. According to these methods, a PCR product is transferred into a vector in **vivo** using a site-specific **recombination** system. In some embodiments, the methods include the steps of (1) providing a PCR product flanked by a first site-specific **recombination** site and a second site-specific **recombination** site; and (2) transferring the PCR product into a cell comprising a target sequence flanked by a first **recombination** site partner and a second **recombination** site partner, and at least one **recombination** protein that mediates **recombination** between the first site-specific **recombination** site and the first **recombination** site partner, and between the second site-specific **recombination** site and the second **recombination** site partner.
TI Method for **cloning** PCR products without restriction or ligation enzymes
IN Kahn, Michael L.; **House, Brent L.**
AB In one aspect the invention provides methods for **cloning** polymerase chain reaction (PCR) products without the need for restriction enzymes, ligation enzymes, or DNA purification steps. According to these methods, a PCR product is transferred into a vector in **vivo** using a site-specific **recombination** system. In some embodiments, the methods include the steps of (1) providing a PCR product flanked by a first site-specific **recombination** site and a second site-specific **recombination** site; and (2) transferring the PCR product into a cell comprising a target sequence flanked by a first **recombination** site partner and a second **recombination** site partner, and at least one **recombination** protein that mediates **recombination** between the first site-specific **recombination** site and the first **recombination** site partner, and between the second site-specific **recombination** site and the second **recombination** site partner.
ST integration **recombination** PCR restriction ligation enzyme
IT Proteins
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(IHF (integration host factor); method for **cloning** PCR products without restriction or ligation enzymes)
IT Escherichia coli
Eubacteria
(as expression host; method for **cloning** PCR products without restriction or ligation enzymes)
IT Genetic element
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(attB, attB1 or attB2 site; method for **cloning** PCR products without restriction or ligation enzymes)
IT Genetic element
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(attP, attP2 or attP1 site; method for **cloning** PCR products without restriction or ligation enzymes)
IT **Recombination**, genetic
(integration; method for **cloning** PCR products without restriction or ligation enzymes)
IT Coliphage λ
Genetic vectors
Genome

Molecular **cloning**
PCR (polymerase chain reaction)
Plasmids
(method for **cloning** PCR products without restriction or ligation enzymes)

IT Primers (nucleic acid)
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(method for **cloning** PCR products without restriction or ligation enzymes)

IT 52350-85-3P, Integrase
RL: BPN (Biosynthetic preparation); BUU (Biological use, unclassified); BIOL (Biological study); PREP (Preparation); USES (Uses)
(method for **cloning** PCR products without restriction or ligation enzymes)

IT 740984-78-5 740984-79-6 740984-80-9 740984-81-0
RL: PRP (Properties)
(unclaimed nucleotide sequence; method for **cloning** PCR products without restriction or ligation enzymes)

L10 ANSWER 3 OF 4 CAPLUS COPYRIGHT 2006 ACS on STN DUPLICATE 2
AN 2004:434419 CAPLUS
DN 141:48120
TI New **recombination** methods for Sinorhizobium meliloti genetics
AU **House, Brent L.**; Mortimer, Michael W.; Kahn, Michael L.
CS Institute of Biological Chemistry and School of Molecular Biosciences, Washington State University, Pullman, WA, 99164-6340, USA
SO Applied and Environmental Microbiology (2004), 70(5), 2806-2815
CODEN: AEMIDF; ISSN: 0099-2240
PB American Society for Microbiology
DT Journal
LA English
AB The availability of bacterial genome sequences has created a need for improved methods for sequence-based functional anal. to facilitate moving from annotated DNA sequence to genetic materials for analyzing the roles that postulated genes play in bacterial phenotypes. A powerful **cloning** method that uses lambda integrase **recombination** to **clone** and manipulate DNA sequences has been adapted for use with the gram-neg. α-proteobacterium Sinorhizobium meliloti in two ways that increase the utility of the system. Adding plasmid oriT sequences to a set of vehicles allows the plasmids to be transferred to S. meliloti by conjugation and also allows **cloned** genes to be recombined from one plasmid to another in **vivo** by a pentaparental mating protocol, saving considerable time and expense. In addition, vehicles that contain yeast Flp recombinase target **recombination** sequences allow the construction of deletion mutations where the end points of the deletions are located at the ends of the **cloned** genes. Several deletions were constructed in a cluster of 60 genes on the symbiotic plasmid (pSymA) of S. meliloti, predicted to code for a denitrification pathway. The mutations do not affect the ability of the bacteria to form nitrogen-fixing nodules on Medicago sativa (alfalfa) roots.
RE.CNT 26 THERE ARE 26 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT
TI New **recombination** methods for Sinorhizobium meliloti genetics
AU **House, Brent L.**; Mortimer, Michael W.; Kahn, Michael L.
AB The availability of bacterial genome sequences has created a need for improved methods for sequence-based functional anal. to facilitate moving from annotated DNA sequence to genetic materials for analyzing the roles that postulated genes play in bacterial phenotypes. A powerful **cloning** method that uses lambda integrase **recombination** to **clone** and manipulate DNA sequences has been adapted for use with the gram-neg. α-proteobacterium Sinorhizobium meliloti in two ways that increase the utility of the system. Adding plasmid oriT sequences to a set of vehicles allows the plasmids to be transferred to S. meliloti by conjugation and also allows **cloned** genes to be recombined from one plasmid to another in **vivo** by a pentaparental mating protocol, saving considerable time and expense. In addition, vehicles that contain yeast Flp recombinase target

recombination sequences allow the construction of deletion mutations where the end points of the deletions are located at the ends of the **cloned** genes. Several deletions were constructed in a cluster of 60 genes on the symbiotic plasmid (pSymA) of S. meliloti, predicted to code for a denitrification pathway. The mutations do not affect the ability of the bacteria to form nitrogen-fixing nodules on Medicago sativa (alfalfa) roots.

ST genetic **recombination** conjugation deletion FLP integrase oriT plasmid Sinorhizobium

IT Enzymes, biological studies
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(DNA-recombining, gene FLP; genetic **recombination**-based methods and tools for **cloning** and constructing deletion mutants in Sinorhizobium meliloti)

IT Genetic element
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(FRT (Flp recombinase target) sequence; genetic **recombination**-based methods and tools for **cloning** and constructing deletion mutants in Sinorhizobium meliloti)

IT Mutagenesis
(deletion; genetic **recombination**-based methods and tools for **cloning** and constructing deletion mutants in Sinorhizobium meliloti)

IT Conjugation (genetic)
Molecular **cloning**
Plasmid vectors
Recombination, genetic
Sinorhizobium meliloti
(genetic **recombination**-based methods and tools for **cloning** and constructing deletion mutants in Sinorhizobium meliloti)

IT Genetic element
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(oriT, use for plasmid mobilization; genetic **recombination**-based methods and tools for **cloning** and constructing deletion mutants in Sinorhizobium meliloti)

IT 52350-85-3, Integrase
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(from λ; genetic **recombination**-based methods and tools for **cloning** and constructing deletion mutants in Sinorhizobium meliloti)

L10 ANSWER 4 OF 4 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:610609 CAPLUS
DN 139:160795
TI Methods and vectors for facilitating site-specific **recombination**
IN Kahn, Michael L.; **House, Brent L.**; Mortimer, Michael W.
PA Washington State University Research Foundation, USA
SO PCT Int. Appl., 52 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 2003064623	A2	20030807	WO 2003-US3176	20030131
WO 2003064623	A3	20040318		

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES,

FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

US 2003219902 A1 20031127 US 2003-357268 20030131

PRAI US 2002-354063P P 20020131

AB Te invention provides methods for moving an insert nucleic acid mol. between vectors using site-specific **recombination** in **vivo**. In another aspect, the invention provides methods for the functional anal. of a genome using site-specific **recombination** in **vivo**. Another aspect of the invention provides methods for deleting a target genomic region by intra-mol. site-specific **recombination**. Further aspects provide vectors and kits for use in the methods of the invention. The invention provides methods and vectors for analyzing a genome of bacteria such as Sinorhizobium meliloti by site-specific **recombination** in-**vivo**. The **recombination** sites comprise FRT sequences and the **recombination** proteins comprise a Flp recombinase. The prototypical site-specific **recombination** is used to integrate bacteriophage λ into E. coli genome.

TI Methods and vectors for facilitating site-specific **recombination**

IN Kahn, Michael L.; **House, Brent L.**; Mortimer, Michael W.

AB Te invention provides methods for moving an insert nucleic acid mol. between vectors using site-specific **recombination** in **vivo**. In another aspect, the invention provides methods for the functional anal. of a genome using site-specific **recombination** in **vivo**. Another aspect of the invention provides methods for deleting a target genomic region by intra-mol. site-specific **recombination**. Further aspects provide vectors and kits for use in the methods of the invention. The invention provides methods and vectors for analyzing a genome of bacteria such as Sinorhizobium meliloti by site-specific **recombination** in-**vivo**. The **recombination** sites comprise FRT sequences and the **recombination** proteins comprise a Flp recombinase. The prototypical site-specific **recombination** is used to integrate bacteriophage λ into E. coli genome.

ST Escherichia plasmid RK2 oriT sequence **cloning** vector **recombination**

IT Plasmids
(ColE1; methods and vectors for facilitating site-specific **recombination**)

IT Enzymes, biological studies
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(DNA-recombining, gene FLP; methods and vectors for facilitating site-specific **recombination**)

IT Genetic element
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(FRT sites; methods and vectors for facilitating site-specific **recombination**)

IT Gene, microbial
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(FRT; methods and vectors for facilitating site-specific **recombination**)

IT Proteins
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(IHF (integration host factor); methods and vectors for facilitating site-specific **recombination**)

IT Plasmids
(RK2; methods and vectors for facilitating site-specific **recombination**)

IT Proteins
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(Xis; methods and vectors for facilitating site-specific **recombination**)

IT Genetic element
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(attB, attB2; methods and vectors for facilitating site-specific **recombination**)

IT Genetic element
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(attL, attL2; methods and vectors for facilitating site-specific

recombination)
IT Genetic element
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(attP, attP1 an attP2 sites; methods and vectors for facilitating site-specific **recombination**)
IT Genetic element
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(attR, attR1 and attR2 site; methods and vectors for facilitating site-specific **recombination**)
IT Genetic element
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(attenuator; methods and vectors for facilitating site-specific **recombination**)
IT Gene, microbial
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(ccdB; methods and vectors for facilitating site-specific **recombination**)
IT **Recombination**, genetic
(homologous; methods and vectors for facilitating site-specific **recombination**)
IT Coliphage λ
Conjugation (genetic)
DNA sequences
Escherichia coli
Eubacteria
Genetic vectors
Molecular **cloning**
Prokaryota
Recombination, genetic
Sinorhizobium meliloti
Test kits
(methods and vectors for facilitating site-specific **recombination**)
IT DNA
Nucleic acids
Promoter (genetic element)
Reporter gene
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(methods and vectors for facilitating site-specific **recombination**)
IT Genetic element
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(oriT, of plasmid RK2; methods and vectors for facilitating site-specific **recombination**)
IT **Recombination**, genetic
(site-specific; methods and vectors for facilitating site-specific **recombination**)
IT 573748-79-5, DNA (Escherichia coli plasmid RK2)
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(nucleotide sequence; methods and vectors for facilitating site-specific **recombination**)
IT 573767-79-0 573767-80-3 573767-81-4 573767-82-5
RL: PRP (Properties)
(unclaimed nucleotide sequence; methods and vectors for facilitating site-specific **recombination**)

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